EXHIBIT 8

UNITED STATES DEPARTMENT OF COMMERCE
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SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKETT NO.

EXAMINER	

ART UNIT	PAPER NUMBER
	10

DATE MAILED:

EXAMINER INTERVIEW SUMMARY RECORD

All participants (applicant, applicant's representative, PTO personnel):

(1) Mr. Danny Huntington, Applicants Counsel (3) Mr Brian Barrett, Applicant Counsel

(2) William W. Moore, Examiner (4) _____

Date of interview 11 January 2001

Type: ☐ Telephonic ☑ Personal (copy is given to ☐ applicant ☐ applicant's representative).

Exhibit shown or demonstration conducted: ☐ Yes ☑ No. If yes, brief description: _____

Agreement ☑ was reached with respect to some or all of the claims in question. ☐ was not reached.

Claims discussed: all pending claims

Identification of prior art discussed: None.

Description of the general nature of what was agreed to if an agreement was reached, or any other comments: It was agreed that cancellation of claim 28 would place all pending claims in condition for allowance and that conditions are met for an interference based upon Applicant's proposed count of Paper No. 9 including claims of all three Foster et al. patents cited in Paper No. 9.

(A fuller description, if necessary, and a copy of the amendments, if available, which the examiner agreed would render the claims allowable must be attached. Also, where no copy of the amendments which would render the claims allowable is available, a summary thereof must be attached.)

☐ 1. It is not necessary for applicant to provide a separate record of the substance of the interview.

Unless the paragraph below has been checked to indicate to the contrary, A FORMAL WRITTEN RESPONSE TO THE LAST OFFICE ACTION IS NOT WAIVED AND MUST INCLUDE THE SUBSTANCE OF THE INTERVIEW (e.g., items 1-7 on the reverse side of this form). If a response to the last Office action has already been filed, then applicant is given one month from this interview date to provide a statement of the substance of the interview.

☐ 2. Since the examiner's interview summary above (including any attachments) reflects a complete response to each of the objections, rejections and requirements that may be present in the last Office action, and since the claims are now allowable, this completed form is considered to fulfill the response requirements of the last Office action. Applicant is not relieved from providing a separate record of the substance of the interview unless box 1 above is also checked.

William W. Moore
Examiner's Signature

PTOL-413 (REV. 2 -93)

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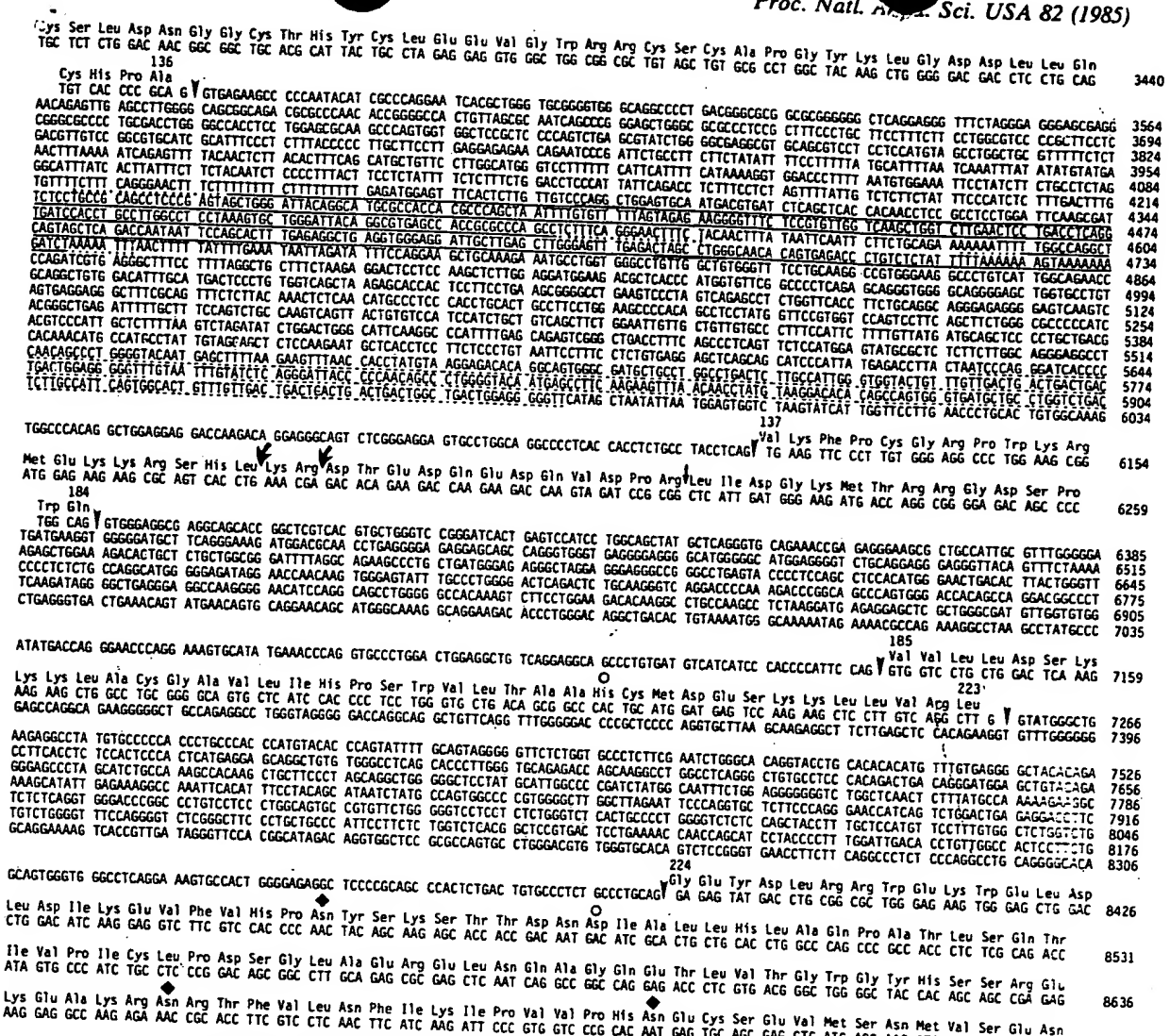

FIG. 2. Nucleotide sequence for the gene for human protein C. The first base of the methionine codon where translation is initiated is numbered +1. Arrowheads indicate intron–exon splice junctions. The two *Alu* sequences in intron E have been underlined with a solid line; the 18-base repeats flanking the first *Alu* sequence and the 8-base repeats flanking the second *Alu* sequence have been underscored with dots. The highly conserved sequences of C-C-A-G-C-C-T-G-G have been underlined with a heavy solid line, contrasting with the two homologous 160-bp repeats in intron E which have been lightly underlined. The polyadenylylation or processing sequences of A-T-T-A-A-A and A-A-T-A-A-A at the 3′ end are boxed. The consensus of C-T-T-T-G, which also may be involved in polyadenylylation or cleavage of mRNA at the 3′ end, is underlined with a wavy line. ◆, Potential carbohydrate binding sites to asparagine residues; ↓, site of cleavage in the heavy chain when protein C is converted to activated protein C; ○, active site aspartic acid, histidine, and serine residues; ●, sites of polyadenylylation.

DNA sequence overlapping the two *Eco*RI junctions between the three fragments, two *Bgl* II fragments of 3.3 and 7.0 kb were isolated and subcloned into the *Bam*HI site of pUC9. These two clones span the *Eco*RI sites.

A detailed restriction map as well as approximate placement of the exon regions within the subcloned fragments were established by further restriction analysis and Southern blotting (Fig. 1). When the 5′ and 3′ ends of the gene were established, the nucleotide sequence of the gene was determined by the dideoxy chain-termination method using nuclease *BAL*-31 to provide overlapping sequences between the ends of large restriction fragments.

The nucleotide sequence for the gene for human protein C spans ≈11 kb of DNA (Fig. 2). Comparison of the genomic sequence with that of the cDNA (9) revealed that the gene consists of eight exons ranging in size from 25 to 885 nucleotides and seven introns ranging in size from 92 to 2668 nucleotides. An additional intron(s) in the 5′ noncoding region cannot be ruled out because a cDNA covering this region was not available for comparison with the gene. Also,